Amendments to the Specification:

Please replace the paragraph [00123] with the following paragraph:

[00123] ABCA1 gene expression is measured using TaqMan quantitative PCR using the following primers/probe set for human ABCA1, forward 5'TGTCCAGTCCAGTAATGGTTCTGT3' (SEQ ID NO. 1), reverse 5'AAGCGAGATATGGTCCGGATT3'(SEQ ID NO. 2), probe 5'FAM AC*ACCTGGAGAGAAGCTTTCAACGAGACTAACC*TAMRA3' (SEQ ID NO. 3), and human 36B4, forward 5'CCACGCTGCTGAACATGC3' (SEQ ID NO. 4), reverse 5'TCGAACACCTGCTGGATGAC3' (SEQ ID NO. 5), probe 5'VIC AACATCTCCCCCTTCTCCTTTGGGCT TAMRA3' (SEQ ID NO. 6). Reverse transcription and PCR reactions are run in sequence in the same sample mixture using the Superscript Platinum III Q-PCR reagent (Invitrogen). Reaction mixes (Superscript RT/ platinum Taq - 0.4µl, 2x Reaction Mix - 10µl, 36B4 primers - 0.4µl of 10µM stock, ABCA1 primers - 1.8µl of 10µM stock, ABCA1 probe-FAM - 0.04µl of 100µM stock, 36B4 probe-VIC - 0.04µl of 50µM stock, RNA (50ng/µl) - 2µl, 50x ROX dye - 0.4µl, MgSO4 - 0.4µl of 50mM stock, water - 4.52µl) are placed in a 384-well plate and run on an ABI HT7900 machine using standard conditions. ABCA1 gene expression is evaluated in reference to a curve of diluted RNA, and normalized to the levels of 36B4 RNA present in the sample. Fold induction induced by compound is calculated in reference to DMSO. Relative efficacy (or percent efficacy) is calculated by comparison of the response elicited by the compound with the maximum value obtained for the known LXR modulator, (3-{3-[(2-Chloro-3-trifluoromethyl-benzyl)-(2,2-diphenyl-ethyl)-amino]-propoxy}-phenyl)-acetic acid.

Please replace the paragraph [00124] with the following paragraph:

[00124] Human HepG2 cells are grown in propagation media (10% FBS, 2mM L-glutamine, 1.5g/L bicarbonate, 0.1mM non-essential amino acids, 1.0mM sodium pyruvate in DMEM). On day 1, 0.5 mL of cells in propagation media at a concentration of 150,000 cells/mL are plated per well on a 48-well plate. Plate is then incubated at 37 degrees for 24 hours. On day 2, media is changed to 0.5 mL of assay media (same as propagation media but with 2% lipoprotein deficient FBS as the serum supplement) and compounds are added 6 hours later (1 or

10μM in DMSO). Plate is then incubated at 37 degrees for 36-48 hours. Cells are harvested and RNA is isolated using the RNeasy kit (Qiagen) with DNaseI option. RNA is eluted in 100ul of water, quantitated (UV absorbance at 260nm) and stored at -80 degrees till use. Fas gene expression is measured using TaqMan quantitative PCR using the following primers/probe set for human Fas, forward 5'GCAAATTCGACCTTTCTCAGAAC3' (SEQ ID NO. 7), reverse 5'GGACCCCGTGGAATGTCA3' (SEQ ID NO. 8), probe 5'FAM ACCCGCTCGGCATGGCTATCTTC TAMRA3' (SEQ ID NO. 9) and human 36B4, forward 5'CCACGCTGCTGAACATGC3' (SEQ ID NO. 10), reverse 5'TCGAACACCTGCTGGATGAC3' (SEQ ID NO. 11), probe 5'VIC AACATCTCCCCCTTCTCCTTTGGGCTTAMRA3' (SEQ ID NO. 12). Reverse transcription and PCR reactions are run in sequence in the same sample mixture using the Superscript Platinum III Q-PCR reagent (Invitrogen). Reaction mixes (Superscript RT/ platinum Taq - 0.4μl, 2x Reaction Mix - 10μl, 36B4 primers – 1.2μl of 10μM stock, Fas primers - 1.2μl of 10μM stock, Fas probe-FAM - 0.045μl of 100μM stock, 36B4 probe-VIC - 0.08μl of 50μM stock, RNA (50ng/μl) - 2μl, 50x ROX dye - 0.4μl, MgSO4 - 1μl of 50mM stock, water – 3.68μl) are placed in a 384-well plate and run on an ABI HT7900 machine with standard conditions. Fas gene expression is evaluated in reference to a curve of diluted RNA, and normalized to the levels of 36B4 RNA present in the sample. Fold induction induced by compound is calculated in reference to DMSO.

Please replace the paragraph [00126] with the following paragraph:

[00126] Fusion proteins, amino acids 205-447 (Genbank NM_005693) for LXRα (NR1H3) and amino acids 203-461 (NM_007121for β) for LXRβ (NR1H3), were cloned in-frame at the Sal1 and Not1 sites of pGEX4T-3 (27-4583-03 Amersham Pharmacia Biotech). A biotinylated peptide sequence was derived from SRC-1 (amino acids 676 to 700): biotin-CPSSHSSLTERHKILHRLLQEGSPSC-OH (SEQ ID NO. 13).